Abstract

Saccharomyces cerevisiae is a unicellular eukaryotic organism capable of forming organized multicellular communities - colonies and biofilms. During development, colonies of laboratory strains differentiate into specifically localized cell subpopulations - U and L cells, located in the upper and lower part of the colony, respectively. The U and L subpopulations of cells vary in morphology, metabolic processes and stress resistance.

Protein granules are membrane-less "organelles" found in both unicellular and multicellular eukaryotic organisms. The formation of protein granules is related to the physiological state of the cell (e.g. chronological and replicative aging), but also to changing environmental conditions and to cellular responses to stress factors. A relatively large fraction of proteins relocalizes to some type of protein granule during the lifespan of the cell. Granule formation can increase fitness of cells, help them to cope with limiting energy resources, and plays a crucial role in the adaptation of cells to stress conditions. Localization of many proteins in the cell varies depending on its physiology. Therefore the specific localization of such proteins may be considered as a "marker" of a specific physiological condition. There are proteins in each type of granule that can be considered as specific "protein markers" of that type of granule.

In this work, a pilot analysis of the occurrence, formation and appearance of protein granules in different types of yeast cells was performed *in situ* in colonies at different stages of their development. A series of *S. cerevisiae* strains with GFP labelled marker proteins of seven different types of granules was prepared for this analysis.

Key words: *Saccharomyces cerevisiae*, colony differentiation, protein granules, P-bodies, stress granules, actin bodies, CUPS, HSP42-SPG, metabolic granules, glycolytic bodies